Access DB#39046

SEARCH REQUEST FORM

Scientific and Technical Information Center

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equester's Full Name: Phone Number 30			le): PAPER DISK E-MAIL
t Unit: Phone Number 30 all Box and Bldg/Room Location:	Results Fo	ormat Preferred (cuc	le): PAPER DIOIE D
		of	need
more than one search is submitted, plea	se prioritize se	arches in order or	need. ******************** subject matter to be searched.
more than one search is ******************** *************	****	cifically as possible the	subject matter to be searched.
ease provide a detailed statement of the search topic	, and describe as spe	and registry numbers, a	nd combine with the concept or
clude the elected species of sudctatos, and	ve a special meaning	. Give examples of ici	evant citations, authors, etc, ii
ease provide a detailed statement of the seath topic clude the elected species or structures, keywords, sy ility of the invention. Define any terms that may ha nown. Please attach a copy of the cover sheet, pertin	ent claims, and abstr	act.	
itle of Invention:			
Earliest Priority Filing Date:			day members) along with the
Earliest Priority Filing Date: *For Sequence Searches Only* Please include all pertin	ent information (pare	nt, child, divisional, or is:	sued patent numbers) with
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alian Time: 2 - 2 - 1	Other	Outer (speed)	

PTC-1590 (1-2000)

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Maximum Match 100%
Listing first 45 summaries
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x60602	V69740	V22271	T04575	V64257	V83956	X85878	X85877	Q66476	V31505	T08603	X88501	ID
S. cerevisiae ATH1	Nucleotide sequenc	pAT-1 (pSD544). S	Plasmid pAT-1 sequ	Plasmid pPK9/10 DN	Bacterial artifici	Synthetic operon c	Nucleotide sequenc	K. marxianus URA3	Base sequence of D	URA3 gene. Candid	A. gossypii orotid	Description

15-JAN-1998;

98DE-1001120

	Rice beta-glucanas	X33535	20	0.182	2.8	38.6	4	
	Rice Gns7	X33569	20	1008		38.6	44	
	Rice beta	X33559	20	933	2.8	38.6	43	
	Rhizobium	V30459	19	536165		39.8	42	
		V30458	19	534720		39.8	41	
	Deleya halophila m	V81457	20	753		39.8	40	
	Sequence of the Ta	N70493	æ	444		75.8	39	
	Human colon cancer	A16205	21	504		95.6	38	
	A. nidulans PCR de	V72393	20	2229		114.2	37	
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		V61459	19	7432	8.	115.2	35	
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	d.	A26728	21	7175	19	270	3	
	Plasmid	A26729	21	6640		273.2	32	
	Pichia p	Q29938	13	2688	21	289.4	31	
	Candida	Q05865	11	906	24.	336.4	30	
		Q05864	11	1220	25.	349	29	
		N90096	10	6978	25.	349.6	28	O
		V19462	19	1179	25.	351.2	27	
	URA3-J Allele (sel	Q71368	15	1115	25.	352.8	26	
	S. cerevisiae URA3	x60601	20	804	25.	355	25	
	Saccharomyces cere	Z07052	20	804	25.	355	24	
	URA3. Saccharomyc	V36432	19	804	25.7	355	23	
	Nucleic acid seque	V23013	19	8140	25.	356	22	
	Yeast expression p	Z27543	20	7633	25.	356	21	O
	Plasmid pSF248 enc	V34061	19	7358	25.	356	20	a
	Nucleotide sequenc	X31837	20	7333	25.	356	19	
	Nucleotide sequenc	X31836	20	7102	25.	356	18	
	Recombinant C reac	Z86938	21	5848	25.	356	17	
	Yeast expression v	V50471	19	5848	25.	356	16	
	tide sequer	V69741	20	4933	25.	356	15	
		V22272	19	4933	25.	356	14	
	Plasmid pAT-2 sequ	T04569	16	4933	25.	356	13	

ALIGNMENTS

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Orotldine-5-phosphate decarboxylase; selectable marker; blosynthesis; Metschnokowiaceae; regulatory activity; chemical blosynthesis; secondary metabolite blosynthesis; protein blosynthesis; flavouring; growth factor; perfume; enzyme blosynthesis; riboflavin; vitamin B2; nutritional supplement; food dye; ss.
                                                                                                                                            CDS
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                               15-JAN-1998;
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                                                                                                           3'UTR
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Best Local :
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       This represents the base sequence of DNA fragment containing yeast URA3 gene. This can be used in the consrtruction of a yeast vector for multi-copying on to chromosomes of yeast such as Candida utilis. The
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vector contains a DNA homologous with a chromosomal gene

of the yeast

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(preferably ribosomal DNA (rDNA) such as the URA3, L41, PGK, GAP or PMA gene), a marker gene to be used in transformant selection (such as a drug resistance gene, e.g. the cycloheximide resistance gene L41, the G418 resistance gene Tm903-APT, or the hygromycin B resistance gene (from E.coll) HPT), a shortened promoter sequence such as the C.utilis L41, phosphoglycerate kinase (PGK), glyceraldehyde-3-phosphate dihydrogenase (GAP) or plasma membrane proton ATPase (PMA) gene promoter and a gene of interest from yeast or other origin. The vectors are useful in the preparation of proteins for food or drug use in high efficiency. They can be used especially for the production of single-chain monellin, which is a low-calorie sweetener whose thermostability is greater than that of the dimeric natural monellin. Multiple copies of the desired gene are integrated into the yeast chromosome and high expression efficiency
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Sequence 2330 BP; 669 ? 498 C 613 G; 550 T; 0 other;

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NO. 1.9e-96;
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ccttgatgtgcggacgtctagaaagcttctggagctagcagacacgctgggaccgccat

tcttgatgttcgtaaaacagcagagttgttaagattagttgaggttttgggtccatatat

gccagttgctagaaagcttctggcattgatgcacgagaagaaaaccaatctctgcgcttc aactaatcaaaggaggatgtcgactaagagttactcggaaagagcagctgctcatagaag

tccagttgctgccaagcttttaaacttgatggaagaagaagtcaaacttatgtgcttc

649 313 Ma. Local 534;

Similarity

26.8%; 66.1%;

Score 369.6; Pred. No. 2.

Conservative

0;

Mismatches

. 2.6e-96; tches 274;

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DB 15;

Length

acctagccattgccacatgtcaacgaaatcttacgcagaaagggccaaaggcacacaattc

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Polymerase chain reaction; primer; amplify; PCR; extension assay; functionality; inulinase; promoter; regulatory region; promoter; upstream activating sequence; upstream repressing sequence; UAS; terminator; secretory signal; secretion; yeast; transformation; protein; metabolite; ss.
                                This sequence represents URA3 gene from K. marxianus. This gene was used in an example in the construction of the uracil requiring K. anus mutants, KMS3. This gene is involved in the regulation of the biosynthesis of pyrimidine. Yeast cells whihe have an active URA3 gene are unable to grow in medium contlaining 5-fluoro-orotic acid (5-FOA). KMS3 is a non-reverting K. marxianus leu2 strain which is suitable for overexpression of homologous or heterologous proteins is the food of the contraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q66476 standard;
                                                                                                                                       Example 13; Fig 12; 68pp; English
                                                                                                                                                                                                                                                                  (UNIL ) QUEST
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29-JAN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K. marxianus URA3
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Sequence 1469 BP; 443 A; 258
                                                                                                                                                                RNA or metabolite
                                                                                                                                                                              Yeast regulatory sequence from the inulinase
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T; 0 other;
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Cameron
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                            (WISC
                                                                                 30-NOV-1998;
                                                                                                                                    WO9928481-A1
                                                                                                                                                                                         organic acid; animal feed; ss.
                                                                                                                                                                                                                                                         Nucleotide sequence of plasmid YEp352.
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Best Local
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                 gcagagctctcttctcagggctcttttggcgcgcggagactataccgcggggcgtcgttgaa
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                                                                                                                                                                                                                                             cgtatcgcggagtgggggatattaccaatgcacacggcgtcaccggccccggtgtgata
                                                                       GCAGAATTGTCATGCAAGGGCTCCCTATCTACTGGAGAATATACTAAGGGTACTGTTGAC
                                                                                                                                                                                                                                                                                                   GACAGAAAATTTGCTGACATTGGTAATACAGTCAAATTGCAGTACTCTGCGGGTGTATAC
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                                                                                                                                                                                                                           AGAATAGCAGAATGGGCAGACATTACGAATGCACACGGTGTGGTGGGCCCCAGGTATTGTT
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                                                                                  The present sequence represents a synthetic operon, comprising CC sequences encoding methylglyoxal synthase (MGS), which is functional CC in yeast cells. It is used in the course of the invention. The CC specification describes a method for the production of ethanol CC and 1,2-propanediol (1,2-pD) comprising using a genetically modified CC yeast which expresses suitable enzymes, particularly an E. coli CC process synthase (MGS). The microbial process can use as a CC substrate a renewable sugar such as glucose, xylose or lactose or products from corn and cane sugar and from lignocellulosic biomass. The products from corn and cane sugar and from lignocellulosic biomass. The products are produced in the production of the production of 1,2-pD which can be used in the production of 1,2-pD which can be used in the production of 1,2-pD which can be used in the production of unsaturated polyester cresins, liquid laundry detergents, pharmaceuticals, cosmetics, antifreeze and delaing formulations. They can also be used to produce ethanol. The byproducts of fermentation are carbon dioxide, alcohols, and organic capters feed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methylglyoxal synthase; MGS; ethanol production; 1,2-propanediol; unsaturated polyester resin; liquid laundry detergent; cosmetic; antifreeze; deicing formulation; carbon dioxide; alcohols;
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                  taccgcaaggccggttgggaggcttacttgcgccgtatgggcgag
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                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a bacterial artificial chromosome (BAC) contig, and exemplifies the invention. The specification describes contiginated acid sequences derived from a eukaryotic chromosome, including a neocentromere or its functional derivative or hybrid, that are able, in a compatible cell, of replicating, acting as extra-chromosomal element can degregating during cell division. The sequences can be used to construct artificial chromosomes for use in gene therapy comprising a creplicable, segregating nucleic acid that confers a specific phenotype con cells. Human artificial chromosomes for use in gene therapy comprising a creplicable, segregating nucleic acid that confers a specific phenotype con cells. Human artificial chromosomes can propagate in human cells and carry large amounts of DNA (e.g. therapeutic genes), and, being carra-chromosomal, they are not mutagenic. The artificial chromosomes can ealso useful for generation of transgenic plants and animals, in compression of cytokines, receptors and growth factors, or to increase the copy number of a gene in a cell. The constructs may also be
                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid comprising neocentromere sequences from eukaryotic chromosome - used to produce replicable, segregating artificial chromosomes that can carry large amounts of DNA for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yeast artificial chromosome; YAC; probe; eukaryotic chromosome; neocentromere; replication; extra-chromosomal element; segregation; cell dlv4slon; artificial chromosome; pene therapy; BAC; transgenic; human artificial chromosome; bacterial artificial chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-AUG-1997;
13-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cancilla MR,
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1101 BP; 351 A; 182 C; 257 G; 311 T; 0 other;
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                  acatgtcgacatactgacggacttcgacatcgagacggcagtcaagccgctgcagct 448
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                                                                             caccaaggaattactggagttagttgaagcattaggtcccaaaatttgtttactaaaaac
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acatgtggatatcttgactgatttttccatggagggcacagttaagccgctaaaggcatt
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97AU-0006784.
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Pred. No. 1.8e-92;
0; Mismatches 275;
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 Entian K,
Kramer W,
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                                                                                                                                                                                                                                                                         Antimycotic agent; target; medicine; infection; veterinary; fungicide; immunodepression; preservative; food industry; fungi; ss.
                                                                                                                                                                                                                                                                                                                   Plasmid pPK9/10 DNA
                                                                                                                                                                                                                                                                                                                                                                           V64257;
                                                                                                                                                                                                                                                                                                                                                                                                       V64257 standard; DNA; 4102 BP
Identification of antimycotic agents using essential fungal proteins or genes as targets - useful, e.g. for potential clinical, human or
                                                                                                                                      02-APR-1997;
                                                                                                                                                                02-APR-1998;
                                                                                                                                                                                            08-OCT-1998.
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                                                                                                         (FARH ) HOECHST AG.
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                                                                 Feldmann H,
Munder T, 1
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                                                                      Rose
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                                                                      Schuster T,
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Zimmermann
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mermann FK;
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or genes as targets

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Matches 521;
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Best Local :
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929 gggaagagaccccaaggtcgagggtgcccgctaccgcaaggccggttgggaggcttactt
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                                                                                                                                         9ACCCC999999Lt99cct99acgacaaaggagacggcct9ggccagcagtaccgcacggt
                                        ggatgatgtggtctctacaggatctgacattattattgttggaagaggactatttgcaaa
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65.5%;
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Pred. No. 3.4e-92;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4164 BP; 1185 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing and genome mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 44-46; 83pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAR-1995;
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Chimeric Escherichia co
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acatgtcgacatactgacggacttcgacatcgagacgacagtcaagccgctgcagcagct
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                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                               02-MAR-1995;
02-MAR-1994;
                                                                                                                                                                                                                              Target DNA sequence determination; pAT-1; pSD544; circular; cyclic; ds.
                                                                                                                                                                                                                                                                                                                                                   V22271 standard; DNA; 4164
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WPI; 1998-270435/24
                          Bocke JD,
                                                    (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                      02-MAR-1995;
                                                                                                                                                 17-MAR-1998
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                                                                                                                                                                                                    Synthetic.
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DNA sequencing - using artificial transposon(s) inserted into PT target DNA by incubation with retroviral or retrotransposon PT integrase in vitro

XX Example; Columns 23-28; 38pp; English.

XX The present sequence was used in the development of a novel method CC for the determination of a target DNA sequence. The method CC comprises: (a) incubating target DNA with a retroviral or retrotransposon integrase and an artificial transposon whose termini are substrates for the integrase, to form target DNA CC molecules with quasi-randomly integrated insertions of the artificial transposon; (b) transforming host cells with the CC ansience ontaining target DNA molecules; (c) selecting transposon-containing target DNA from the transformants harbouring transposon-containing target DNA, the primer to complementary to a portion of the artificial transposon; and (f) CC extending the primer to determine a nucleotide sequence flanking CC extending the primer to determine a nucleotide sequence flanking CC is supplied as Tyl virus-like particles. The termini contain Tyl U3 sequences. The termini consist of 4-11 bp. The artificial transposon is provided by digestion with a restriction enzyme that CC generates AACA blunt ends, especially XmnI. Step (b) is effected by electroporation. The molar ratio of artificial transposon to target DNA is at least 2.5:1. Target DNA can be engineered to convert CC virtually any DNA sequence or combination of sequences into an CC feature can be easily designed and constructed.

XX Sequence 4164 BP; 1185 A; 886 C; 988 G; 1105 T; 0 other;
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B Qy δÃ В В 20 Вр Ş В Ω B Qγ В Š В Query Match Best Local Similarity Matches 521; 569 509 656 449 596 389 acatgtcgacatactgacggacttcgacatcgagacgacagtcaagccgctgcagct 448 329 476 269 416 catgtcgaaagctacatataaggaacgtgctgctactcatcctagtcctgttgctgccaa 475 209 aacaaaggaacctagaggccttttgatgttagcagaattgtcatgcaagggctccctatc gtctagaaagcttctggagctagcagacacgctggggaccgcacatttgtctgctgaagac tgcacacggtgtggggcccaggtattgttagcggtttgaagcaggcggcagaagaagt tgcacacygcgtcaccggccccggtgtgatagccgggctgaaggaggctgcgaaactggc agtcaaa!tgcagtactctgcgggtgtatacagaatagcagaatgggcagacattacgaa ggttaagctgcagtactcctccggcgtgtaccgtatcgcggagtgggcggatattaccaa atccgccaagtacaattttttactcttcgaagacagaaaatttgctgacattggtaatac tgcggctaagcacaacttcatgatcttcgaggaccgcaagttcgctgacattggcaacac acatgtggatatcttgactgatttttccatggagggcacagttaagccgctaaaggcatt gctatttaatatcatgcacgaaaagcaaacaaacttgtgtgcttcattggatgttcgtac gcttctggcattgatgcacgagaagaaaaccaatctctgcgcttcccttgatgtgcggac catgtcaacgaaatcttacgcagaaagggccacaggccacaaattcgccagttgctagaaa caccaaggaattactggagttagttgaagcattaggtcccaaaatttgtttactaaaaac Conservative 25.8%; 0; Score 356; DB 19; Pred. No. 3.5e-92; Mismatches 275; Length 4164; Indels 0; Gaps 895 835 508 595 328 715 535

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689 gcgcggagactataccgcgggcgtcgttgaaatggcgaagctggacgaagactttgtgat 748

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comprising a marker gene flanked by terminal sequences, each comprising at least 4 bp of a U3 sequence of yeast retrotransposon Tyl. The DNA molecule used for generating such artificial transposons comprise an origin of replication; a first selectable marker gene; two blunt-ended transposon termini, each of at least 4 bp, that are substrates for yeast retrotransposon Tyl integrase and flank a first restriction site useful for insertion of a second selectable marker gene to form an artificial transposon, and a second restriction site flanking the two transposon
                                                                                                                          This represents the nucleotide sequence of an artificial transposon AT-1 plasmid (pAT-1). The invention provides methods for creating artificial transposons and inserting these transposons into DNA targets in vitro. The artificial transposon consists of a linear blunt-ended DNA molecule
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02-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transposon; artificial; marker gene; U3; Ty1; DNA mapping; DNA sequencing; primer
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                                                                                                                                                                                                                                                 Artificial transposons
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94US-0204675.
96US-0660754.
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 1196
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                                                                                                                                                                                    gacacccggtgtgggtttagatgacaagggagacgcattgggtcaacagtatagaaccgt
                                                                                                                                                                                                                                               cggctttattgctcaaagagacatgggtggaagagatgaaggttacgattggttgattat
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Pred. No. 3.5e-92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acidic trehalase; ATH1 gene; gene manipulation; baker's yeast; dough;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S. cerevisiae ATH1 gene coding region as cleaved with URA3 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New acid trehalase (ATH1) gene-disrupted haploid yeast, useful preparing high-sugar dough resistant to freezing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-DEC-1997;
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1403
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4292 BP; 1385 A; 787 C; 879 G; 1241 T; 0 other;
                                                                                                                                                                                                                                                                                                          209 catgtcaacgaaatcttacgcagaaagggccaaggcacacaattcgccagttgctagaaa 268
                                                                                                                                                                                                                                           269
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                                                                                  acatgtcgacatactgacggacttcgacatcgagacggcagtcaagccgctgcagct 448
                                                                                                                                                                                                      gctatttaatatcatgcacgaaaagcaaacaacttgtgtgcttcattggatgttcgtac 1282
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                                                                                                                                  caccaaggaattactggagttagttgaagcattaggtcccaaaatttgtttactaaaaac
                                                                                                                                                       gtctagaaagcttctggagctagcagacacgctgggaccgcacatttgtctgctgaagac 388
                                                                acatgtggatatcttgactgatttttccatggagggcacagttaagccgctaaaggcatt
atccgccaagtacaattttttactcttcgaagacagaaaatttgctgacattggtaatac 1462
              tgcggctaagcacaacttcatgatcttcgaggaccgcaagttcgctgacattggcaacac
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Pred. No. 3.5e-92;
0; Mismatches 275;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric Saccharomyces cerevisiae;
Chimeric Escherichia coli;
Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pAT-2; plasmid; primer island artificial transposon; PART;
DNA sequencing; mapping; genome; ds; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pAT-2 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T04569;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T04569
                          Disclosure; Fig 9A-C; 83pp; English
                                                                                  In vitro transposition of artificial transposon(s) - useful e.g. for sequencing entire genome(s) of particular organisms
                                                                                                                                                                                                                                                                                                                                                                     02-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9523875-A1.
                                                                                                                                                                                 WPI; 1995-320587/41
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Best Local
                                                                                      1076 ggatgatgtggtctctacaggatctgacattattattgttggaagaggactatttgcaaa
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                                                                                                                                                                                                                                                                                                                                   749
                                                                                                                                                                                                                                                                                                                                                                              968
                                                                                                                                                                                                                                                                                                                                                                                                                                                    836 aacaaaggaacctagaggccttttgatgttagcagaattgtcatgcaagggctccctatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4933 BP; 1431 A; 1031 C; 1157 G; 1314 T; 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA sequencing and genome mapping.
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999aagggatgctaaggtagagggtgaacgttacagaaaagcaggctgggaagcatattt 1195
                            999aagagaccccaaggtcgagggtgcccgctaccgcaaggccggttgggaggcttactt 988
                                                                                                                     99atga99tcgtca9cgacggtaccgatgtgatcattgttggcagaggggctctttgacaa 928
                                                                                                                                                                                                              9acccc99g9gtt9gcct9gacgacaaaggagacggcctgggccagcagtaccgcacggt 868
                                                                                                                                                                                                                                                                                                                                                                tactggagaatatactaagggtactgttgacattgcgaagagcgacaaagattttgttat 955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acatgtggatatcttgactgatttttccatggagggcacagttaagccgctaaaggcatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acatgtcgacatactgacgacttcgacatcgagacggcaggtcaagccgctgcagcagct 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caccaaggaattactggagttagttgaagcattaggtcccaaaatttgtttactaaaaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gctatttaatatcatgcacgaaaagcaaacaaacttgtgtgcttcattggatgttcgtac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          catgtcaacgaaatcttacgcagaaagggccaaggcacacaattcgccagttgctagaaa 268
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Pred. No. 3.7e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 4933;
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1196 gagaagatgcggccag

1211

Db Ş

416

209 catgicaacgaaatcitacgcagaaagggccaaggcacacaattcgccagitgctagaaa 268

catgtcgaaagctacatataaggaacgtgctgctactcatcctagtcctgttgctgccaa 475

Query Match Matches

Local Similarity

25.8%;

521;

Conservative

0,

Score 356; DB 19; Pred. No. 3.7e-92; 0; Mismatches 275;

Length 4933;

Indels

0;

Gaps

989 gcgccgtatgggcgag 1004

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c undeques with quasi-randomny integrated insertions of the artificial transposon; (b) transforming host cells with the C transposon-containing target DNA molecules; (c) selecting transposon-containing target DNA; (d) cc isolating transposon-containing target DNA; (d) cc for use as a DNA sequencing template; (e) hybridising a primer to complementary to a portion of the artificial transposon; and (f) cc the isolated transposon-containing target DNA, the primer being cc complementary to a portion of the artificial transposon; and (f) ct extending the primer to determine a nucleotide sequence flanking ct arguments. The primer to determine a nucleotide sequence flanking ct is supplied as Tyl virus-like particles. The termini contain Tyl U3 csequences. The termini consist of 4-11 bp. The artificial transposon is provided by digestion with a restriction enzyme that concernts and buint ends, especially xmnI. Step (b) is effected by clettroporation. The molar ratio of artificial transposon to target CDNA is at least 2.5:1. Target DNA can be engineered to convert curificial transposon, so custom transposons having any desired cartificial transposon, so custom transposons and desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
V22272
Sequence 4933 BP; 1431 A; 1031 C; 1157 G; 1314 T;
                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence was used in the development of a novel method for the determination of a target DNA sequence. The method comprises: (a) incubating target DNA with a retroviral or retrotransposon integrase and an artificial transposon whose termini are substrates for the integrase, to form target DNA molecules with quasi-randomly integrated insertions of the artificial transposon.
                                      feature can be easily designed and constructed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Columns 27-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA sequencing - using artificial transposon(s) inserted into target DNA by incubation with retroviral or retrotransposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boeke JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     integrase in vitro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Target DNA sequence determination; pAT-2; pSD545; circular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT-2 (pSD545).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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RESULT 15
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                                                                                                                                                                Nucleotide sequence of artificial transposon AT-2 (pAT-2) plasmid
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                                                                                                                 artificial; marker gene; U3; yeast; retrotransposon;
pping; DNA sequencing; primer site; pAT-2; ds.
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This represents the nucleotide sequence of an artificial transposon AT-2 CC plasmid (pAT-2). The invention provides methods for creating artificial transposons and inserting these transposons into DNA targets in vitro. The artificial transposon consists of a linear blunt-ended DNA molecule CC comprising a marker gene flanked by terminal sequences, each comprising at least 4 bp of a U3 sequence of yeast retrotransposon Tyl. The DNA CC molecule used for generating such artificial transposons comprise an CC origin of replication; a first selectable marker gene; two blunt-ended CC transposon termini, each of at least 4 bp, that are substrates for yeast CC retrotransposon Tyl integrase and flank a first restriction site useful CC transposon, and a second selectable marker gene to form an artificial CC transposon, and a second restriction site flanking the two transposon CC termini, where digestion with the second restriction enzyme liberates a Dlunt-ended fragment having the transposon termini at either end, the CC fragment being an artificial transposon termini at either end, the CC mapping and sequencing of e.g. both functional and non-functional CC sequences, primer sites and restriction sites.
Sequence 4933 BP; 1431 A; 1031 C; 1157 G; 1314 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAR-1995;
02-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Artificial transposons
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing
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94US-0204675.
96US-0660754.
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Ъ DЬ В Ş Вb Ş 맑 Matches Query Match Best Local Similarity 656 449 416 596 389 536 269 209 aacaaaggaacctagaggccttttgatgttagcagaattgtcatgcaagggctccctatc ctcacaggaacccagggggttgctgatgctggcagagctctcttctcagggctcttttggc acatgtcgacatactgacggacttcgacatcgagacgacagtcaagccgctgcagcagct catgtcgaaagctacatataaggaacgtgctgctactcatcctagtcctgttgctgccaa catgtcaacgaaatcttacgcagaaagggccaaggcacaattcgccagttgctagaaa ggttaagctgcagtactcctccggcgtgtaccgtatcgcggagtgggggggtattaccaa atccgccaagtacaattttttactcttcgaagacagaaaatttgctgacattggtaatac tgcggctaagcacaacttcatgatcttcgaggaccgcaagttcgctgacattggcaacac caccaaggaattactggagttagttgaagcattaggtcccaaaatttgtttactaaaaac tgcacacggtgtggtgggcccaggtattgttagcggtttgaagcaggcggcagaagaagt agtcaaattgcagtactctgcgggtgtatacagaatagcagaatgggcagacattacgaa acatgtggatatcttgactgatttttccatggagggcacagttaagccgctaaaggcatt gtctagaaagcttctggagctagcagacacgctgggaccgcacatttgtctgctgaagac gctatttaatatcatgcacgaaaagcaaacaaacttgtgtgcttcattggatgttcgtac gcttctggcattgatgcacgagaagaaaaccaatctctgcgcttcccttgatgtgcggac Conservative 25.8%; 0; Score 356; DB 20; Pred. No. 3.7e-92; 0; Mismatches 275 Length 4933; Indels .. Gaps 895 688 835 715 448 535 475 0

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                               ggatgatgtgtctctacaggatctgacattattattgttggaagaggactatttgcaaa 1135
        gcgccgtatgggcgag 1004
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Search completed: April 4, 2001, 00:03:46 Job time: 7828 sec

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Result
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-441-751-3

PCT-US92-05521-3

US-07-846-181-6

US-07-845-989-6

US-08-232-463-14

US-08-232-463-14

US-08-152-0719A-41
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PCT-US-9-0-550-1
US-08-796-364-2
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2744.339 Million cell updates/sec
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2.5	2.5	2.5	2.5	2.5	2.6	2.6.	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.7
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Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	6	1,	1	Sequence 1, Appli	Sequence 1, Appli	Patent No. 5512669	Patent No. 5229279	Sequence 1, Appli	Sequence 23, Appl	Sequence 3, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 1, Appli

ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: KONDO, Keiji
APPLICANT: KAJIWARA, SUSUMU
APPLICANT: MISAWA, NO. 584952
TITLE OF INVENTION: TRANSFORM
TITLE OF INVENTION: CANDIDA U
TITLE OF INVENTION: THEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08557128 Patent No. 5849524
                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/557,128
FILING DATE: 25-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP95/01005
FILING DATE: 25-MAY-1995
PRIOR APPLICATION NUMBER: JP 7-129287
APPLICATION NUMBER: JP 7-129287
APPLICATION NUMBER: JP 6-285823
APPLICATION NUMBER: JP 6-285823
APPLICATION NUMBER: JP 6-285823
APPLICATION DATA:
APPLICATION NUMBER: JP 6-135015
   TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2330 base pair
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 49
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 3000 K S
CITY: Washington
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3000 K Street, N.W., Suite
2330 base pairs
                                                                                                                       : (202)672-5300
(202)672-5399
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TRANSFORMATION SYSTEMS FOR THE YEAST
CANDIDA UTILIS AND THE EXPRESSION OF HETEROLOGOUS GENES
THEREWITH
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TYPE:

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RESULT 2
US-08-801-344-5/c
; Sequence 5, Application US/08801344
; Patent No. 6087140
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Best Local Similarity
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                                                                                                                                       gagaccccaaggtcgagggtgcccgctaccgcaaggccggttgggaggctta 985
                                                                                                                                                                                                                  aggtegteagegaeggtaeegatgtgateattgttggeagagggetetttgaeaagggaa 933
                                                                                                                                                                                                                                                                                                                                                                          tcatcgcgcagcgtgacatgggtgggcgtgcagacggctttgactggctcatcatgaccc 813
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                                                                                                                   GAGATCCAACAGTGGAAGGTGAGCGTTATAGAAAAGCAGGCTGGGATGCTTA 2037
                                                                                                                                                                                                AGGTTGTCAGTGGTGGCTCTGACATCATCATCGTTGGTAGAGGCTTGTTTGGAAAGGGAA
                                                                                                                                                                                                                                                                             CAGGCGTGGGACTCGACGATAAGGGCGACTCCCTGGGCCAACAGTACAGAACTGTCGATG
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                                                                                                                                                                                                                                                                                                                                                        TCATCGCACAGAGAGACATGGGTGGCAGAGAAGATGGGTTCGACTGGATCATCATGACAC 1865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aggaacccagggggttgctgatgctggcagagctctcttctcagggctcttttggcgcgcg 693
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67.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 370.4; DB 2; Pred. No. 3.3e-101;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cameron, Douglas C. APPLICANT: Shaw, Anita J. APPLICANT: Altaras, Nedim E. APPLICANT: Altaras, Nedim E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
ORGANISM: Yea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: MICROBIAL TITLE OF INVENTION: FROM SUGAR
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                                                                                                                                     1017
                                                                                                                                                                                                                                                                                           1137 GCTACTCATCCTAGTCCTGTTGCTGCCAAGCTATTTAATATCATGCACGAAAAGCAAACA 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1257 ATATACGCATATGTAGTGTTGAAGAAACATGAAATTGCCCAGTATTCTTAACCCAACTGC 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 acatacattctgatggtgtaggctccacatcacagtaagcatttgtataaggctgatcac 179
                     480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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nes 555; Conserv
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gaccgcaagttcgctgacattggcaacacggttaagctgcagtactcctccggcgtgtac
                                                                                                                                     TTAGGTCCCAAAATTTGTTTACTAAAAACACATGTGGATATCTTGACTGATTTTTCCATG
                                                                                                                                                                                                                                                                                                               atagggtgctaccgacctagccattgccacatgtcaacgaaatcttacgcagaaagggcc 239
                                                           GAGGGCACAGTTAAGCCGCTAAAGGCATTATCCGCCAAGTACAATTTTTTACTCTTCGAA
                                                                             gagacgacagtcaagccgctgcagcagcttgcgggctaagcacaacttcatgatcttcgag 479
                                                                                                                                                       ctgggaccgcacatttgtctgctgaagacacatgtcgacatactgacggacttcgacatc 419
                                                                                                                                                                                                                 aatctctgcgcttccccttgatgtgcggacgtctagaaagcttctggaagctagcagacacg
                                                                                                                                                                                                                                                                                                                                                                       ACAGAACAAAAACCGAAACGAAGATAAATCATGTCGAAAGCTACATATAAGGAACGTGCT 1138
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8000 Excelsior Drive, Suite 401
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62.7%;
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pred. No. 5.5e-97; 
0; Mismatches 330; Indels
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                                     INFORMATION FOR SEQ ID NO: 1:
                                                                                 REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202.508.9100
                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                  SEQUENCE CHARACTERISTICS:
                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 100-
CITY: Washington
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                                                 TELEPHONE: 202.508.910
TELEFAX: 202.508.9299
TELEX: 197430 BBMB UT
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                                                                                                                                                                                                                APPLICATION NUMBER: US/01 FILING DATE: 02-MAR-1994
                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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4164 base pairs
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Best Local Similarity
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TOPOLOGY: circular
MOLECULE TYPE: DNA (geno
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: PAT-1
                                                                1136
1196 GAGAAGATGCGGCCAG 1211
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                                                                               gggaagagaccccaaggtcgagggtgcccgctaccgccaaggccggttgggaggcttactt 988
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                                                                GGGAAGGGATGCTAAGGTAGAGGGTGAACGTTACAGAAAAGCAGGCTGGGAAGCATATTT
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; IMMEDIATE SOURCE:
; CLONE: pAT-1
US-08-660-754-1
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TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO:
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APPLICANT:
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HYPOTHETICAL: N
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LENGTH: 4164 base pair
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REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202.508.9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/204,675
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: In Vitro Tr
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              449
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
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tgcggctaagcacatctcatgatcttcgaggaccgcaagttcgctgacattggcaacac
                                                        acatgtcgacatactgacggacttcgacatcgagacgacagtcaagccgctgcagct 448
                                                                                                CACCAAGGAATTACTGGAGTTAGTTGAAGCATTAGGTCCCAAAATTTGTTTACTAAAAAC
                                                                                                               gtctagaaagcttctggagctagcagacacgctgggaccgcacatttgtctgctgaagac
                                                                                                                                                      GCTATTTAATATCATGCACGAAAAGCAAACAAACTTGTGTGCTTCATTGGATGTTCGTAC
                                                                                                                                                                    gcttctggcattgatgcacgagaagaaaaccaatctctgcgcttcccttgatgtgcggac
                                           ACATGTGGATATCTTGACTGATTTTTCCATGGAGGGCACAGTTAAGCCGCTAAAGGCATT
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21; Conservative
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Boeke, Jef D.
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65.5%;
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In Vitro Transposition of Artificial
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                                                                                                                                                                                                                                                               Score 356; DB 2; Length 4164; Pred. No. 9.6e-97; o; Mismatches 275; Indels
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US-08-796-364-1
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                      APPLICATION NUMBER: US 0:
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Devine, Scott E.
APPLICANT: Boeke, Jef D.
APPLICANT: Braiterman, Lelita T.
TITLE OF INVENTION: In Vitro Transposition of Artificial
                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1. CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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CITY: Washington
STATE: D.C.
                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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TELECOMMUNICATION INFORMATION: TELEPHONE: 202.508.9100

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TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4164 base pair
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HYPOTHETICAL: NO
1136 GGGAAGGGATGCTAAGGTAGAGGGTGAACGTTACAGAAAAGCAGGCTGGGAAGCATATTT
                                                                              1076 GGATGATGTGGTCTCTACAGGATCTGACATTATTGTTGGAAGAGGACTATTTGCAAA
                                                                                                                                                            1016 GACACCCGGTGTGGGTTTAGATGACAAGGGAGACGCATTGGGTCAACAGTATAGAACCGT
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                                                                                                   869 ggatgaggtcgtcagcggtaccgatgtgatcattgttggcagagggctctttgacaa 928
                                                                                                                                                                                   809 gaccccgggggttggcctggacgacaaaggagacggcctgggccagcagtaccgcacggt 868
                   929 999aagagaccccaaggtcgagggtgcccgctaccgcaaggccggttgggaggcttactt 988
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                                                                                                                                                                                                                                          CGGCTTTATTGCTCAAAGAGACATGGGTGGAAGAGATGAAGGTTACGATTGGTTGATTAT
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65.5%;
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NAME: Kagan, Sarah A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 0110

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202,508,9100

TELEFAX: 202,508,9299

TELEFAX: 202,508,9299

TELEFAX: 197430 BBMB UT

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 4164 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application PC/TUS9502520 GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University
                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
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HYPOTHETICAL: N
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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                                                                                                                                                                                        476
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COUNTRY: U.
ZIP: 20001
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449 tgcggctaagcacaacttcatgatcttcgaggaccgcaagttcgctgacattggcaacac
                                          596
                                                                                                              536 CACCAAGGAATTACTGGAGTTAGTTGAAGCATTAGGTCCCAAAATTTGTTTACTAAAAAC
                                                                                                                                             329 gtctagaaagcttctggagctagcagacacgctgggaccgcacatttgtctgctgaagac
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                    Local Similarity 65.5 nes 521; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/
FILING DATE: 02-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1001 G St
CITY: Washington
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                                                          acatgtcgacatactgacggacttcgacatcgagacgacagtcaagccgctgcagct 448
                                                                                                                                                                                    GCTATTTAATATCATGCACGAAAAAGCAAACAAACTTGTGTGCTTCATTGGATGTTCGTAC
                                                                                                                                                                                                         catgtcaacgaaatcttacgccagaaagggccaaggcacaattcgccagttgctagaaa 268
                                        ACATGTGGATATCTTGACTGATTTTTCCATGGAGGGCACAGTTAAGCCGCTAAAGGCATT
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65.5%;
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                                                                                                                                                                                                                                                                                                                                  Score 356; DB 4; I Pred. No. 9.6e-97; 0; Mismatches 275;
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US-08-204-675-2
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APPLICANT: Devine,
APPLICANT: Boeke,
APPLICANT: Braiter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Patent No.
CLASSIFICATION: 435
ATTOREY/AGENT INFORMATION:
NAME: Kagen, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202.508.9100
                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Devine, Scott E.
APPLICANT: Boeke, Jef D.
APPLICANT: Braiterman, Lelita T.
TITLE OF INVENTION: In vitro Transposition of Artificial
TITLE OF INVENTION: Transposons
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1196
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001
                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                 APPLICATION NUMBER: US/08/204,675 FILING DATE: 02-MAR-1994
                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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1001 G Street, N.
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Matches 521; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 4933 base pairs
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STRANDEDNESS: double
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TELEX: 197430 BBMB UT
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gcgccgtatgggcgag 1004
                                                               GGGAAGGGATGCTAAGGTAGAGGGTGAACGTTACAGAAAAGCAGGCTGGGAAGCATATTT 1195
                                                                                          gggaagagaccccaaggtcgagggtgcccgctaccgcaaggccggttgggaggcttactt 988
                                                                                                                                                                              GGATGATGTGGTCTCTACAGGATCTGACATTATTATTGTTGGAAGAGGACTATTTGCAAA 1135
                                                                                                                                                                                                         ggatgaggtcgtcagcgacggtaccgatgtgatcattgttggcagagggctctttgacaa
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Pred. No. 1.1e-96;
0; Mismatches 275;
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Best Local :
                                                                                                                                                                                                           Matches 521;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202.508.9100
TELEFAX: 202.508.9299
                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA
HYPOTHETICAL: NO
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Transposons
                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 4933 base pairs
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PRIOR APPLICATION DATA:
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389 acatgtcgacatactgacggacttcgacatcgagacgacagtcaagccgctgcagcagct 448
                              536 CACCAAGGAATTACTGGAGTTAGTTGAAGCATTAGGTCCCAAAATTTGTTTACTAAAAAC 595
                                                                                                                                             416 CATGTCGAAAGCTACATATAAGGAACGTGCTGCTACTCATCCTAGTCCTGTTGCTGCCAA 475
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COUNTRY:
                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                     GCTATTTAATATCATGCACGAAAAGCAAACAAACTTGTGTGCTTCATTGGATGTTCGTAC 535
                                                                                                      gcttctggcattgatgcacgagaagaaaaccaatctctgcgcttcccttgatgtgcggac 328
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VENTION: In Vitro Transposition of Artificial
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                                                                                                                                                                                                                      Score 356; DB 2; Length 4933; Pred. No. 1.1e-96;
                                                                                                                                                                                                          Mismatches 275; Indels
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Sequence 2, Application US/08796364 Patent No. 5968785
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                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Devine, Scott E.
APPLICANT: Boeke, Jef D.
APPLICANT: Braiterman, Lelita T.
TITLE OF INVENTION: In Vitro Transposition of Artificial
TITLE OF INVENTION: Transposons
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                             CLASSIFICATION:
                                                                                        APPLICATION NUMBER: US/08/796,364 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                            STREET: 1001 G STATE: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Banner, Birch, McKie, and Beckett STREET: 1001\ \text{G} Street, N.W.
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  US 08/204,675
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US-08-796-364-2
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Best Local Similarity
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TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202.508.9100
TELEPAX: 202.508.9299
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ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 4933 base pairs
TYPE: nucleic acid
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ggatgaggtcgtcagcgacggtaccgatgtgatcattgttggcagagggctctttgacaa 928
                                                                  GACACCCGGTGTGGGTTTAGATGACAAGGGAGACGCATTGGGTCAACAGTATAGAACCGT 1075
                                                                                        gaccccgggggttggcctggacgacaaaggagacggcctgggccagcagtaccgcacggt 868
                                                                                                                                                                                                                                       TACTGGAGAATATACTAAGGGTACTGTTGACATTGCGAAGAGCGACAAAGATTTTGTTAT 955
                                                                                                                                                                                                                                                           gcgcggagactataccgcgggcgtcgttgaaatggcgaaggctggacgaagactttgtgat 748
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                                                                                                                                                   CGGCTTTATTGCTCAAAGAGACATGGGTGGAAGAGATGAAGGTTACGATTGGTTGATTAT
                                                                                                                                                                                cgggttcatcgcgcagcgtgacatgggtggggcgtgcagacggctttgactggctcatcat 808
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Pred. No. 1.1e-96;
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PCT-US95-02520-2
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GENERAL INFORMATION:
APPLICANT: The Jo
                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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TELEFAX: 202.508.9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: The Johns Hopkins University
TITLE OF INVENTION: In Vitro Transposition of Artificial
TITLE OF INVENTION: Transposons
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Kagan, Sarah A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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536 CACCAAGGAATTACTGGAGTTAGTTGAAGCATTAGGTCCCAAAATTTGTTTACTAAAAAC
                 329 gtctagaaagcttctggaagctagcagacacgctgggaccgcacatttgtctgctgaagac 388
                                                                                                                                                  416 CATGTCGAAAGCTACATATAAGGAACGTGCTGCTACTCATCCTAGTCCTGTTGCTGCCAA 475
                                                                                                                                                                         209 catgtcaacgaaatcttacgcagaaagggccaaggcacacaattcgccagttgctagaaa 268
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OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
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TELEX: 197430 BBMB UT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 02-M
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                                                                                              gcttctggcattgatgcacgagaagaaaaccaatctctgcgcttcccttgatgtgcggac 328
                                                                          GCTATTTAATATCATGCACGAAAAGCAAACAAACTTGTGTGCTTCATTGGATGTTCGTAC
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Pred. No. 1.1e-96;
0; Mismatches 275;
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APPLICANT: Bradley, John D.

APPLICANT: Thompson, Craig M.

APPLICANT: Moore, Jeffrey B.

APPLICANT: Woobe, C. Richard

APPLICANT: Wobbe, C. Richard

APPLICANT: Donneilly, Caroline E.

TITLE OF INVENTION: REGULATED GENE EXPRESSION IN YE,

FILE REFERENCE: 0342/10469US1

CURRENT APPLICATION NUMBER: US/09/138,024A

CURRENT FILING DATE: 1998-08-21

EARLIER APPLICATION NUMBER: 60/056,719

EARLIER FILING DATE: 1997-08-22

MINMAGE OF SEC. 71 NOW. 24
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                                            NUMBER OF SEQ ID NOS: 24
SOFTWARE: FRSTSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 7102
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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FEATURE:
OTHER INFORMATION: Plasmid pzm195
-09-138-024-20
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6594 gagaagatgcggccag 6609
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                                                                      gggaagggatgctaaggtagaggtgaacgttacagaaaagcaggctgggaagcatattt
                                                                                                                                               ggatgatgtggtctctacaggatctgacattattattgttggaagaggactatttgcaaa
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GENERAL INFORMATION:
APPLICANT: Bradley, John D.
APPLICANT: Thompson, Craig M.
APPLICANT: Moore, Jeffrey B.
APPLICANT: Wobbe, C. Richard
APPLICANT: Wobbe, C. Richard
APPLICANT: Donnelly, Caroline E.
TITLE OF INVENTION: REGULATED GE

GENE EXPRESSION

IN YEAST

US-09-138-024-21

Sequence 21, Application US/09138024A Patent No. 6004779

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Matches 521; Conserv
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Best Local (
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LENGTH: 7333
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CURRENT APPLICATION NUMBER: US/09/138,024A
CURRENT FILING DATE: 1998-08-21
EARLIER APPLICATION NUMBER: 60/056,719
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEO ID NOS: 24
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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                                          gggaagggatgctaaggtagagggtgaacgttacagaaaagcaggctgggaagcatattt 6824
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gcgccgtatgggcgag 1004
                                                                   gggaagagaccccaaggtcgagggtgcccgctaccgcaaggccggttggggaggcttactt 988
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Patent No. 6060249
GENERAL INFORMATION:
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Best Local Similarity 65.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 27-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kevin Baker, Austin Gurney
TITLE OF INVENTION: Method of Selection for Genes Encoding
TITLE OF INVENTION: Secreted and Transmembrane Proteins
                                                                                                                                                                                                          3768 CATGTCGAAAGCTACATATAAGGAACGTGCTGCTACTCATCCTAGTCCTGTTGCTGCCAA 3709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                             3708 GCTATTTAATATCATGCACGAAAAGCAAACATTGTGTGCTTCATTGGATGTTCGTAC
                                            3528 ATCCGCCAAGTACAATTTTTTACTCTTCGAAGACAGAAAATTTGCTGACATTGGTAATAC 3469
                                                                                                                                                               389 acatgicgacatactgacggacttcgacatcgagacgacagtcaagccgctgcagcagct 448
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509 ggttaagctgcagtactcctccggcgtgtaccgtatcgcggagtgggcggatattaccaa 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 050, - 9881
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 7633 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39
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CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: Linear
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                                                               tgcggctaagcacaacttcatgatcttccgaggaccgcaagttcgctgacattggcaacac 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 356; DB 3; Length 7633; Pred. No. 1.4e-96;
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Best Local
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LENGTH: 7633
                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kevin Baker, Austin Gurney
TITLE OF INVENTION: Method of Selection for Genes
TITLE OF INVENTION: Transmembrane Proteins
FILE REFERENCE: p1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: p1058
CURRENT APPLICATION NUMBER: US/08/815,520A
CURRENT FILING DATE: 1997-02-27
                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial
FEATURE:
NAME/KEY: Artificial Sequence
LOCATION: 1-7633
COTHER INFORMATION: Amylase yeast expression plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                    3768 CATGTCGAAAGCTACATATAAGGAACGTGCTGCTACTCATCCTAGTCCTGTTGCTGCCAA 3709
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                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                    Score 356; DB 3;
Pred. No. 1.4e-96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application Patent No. 5695961
GENERAL INFORMATION:
                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                     APPLICATION NUMBER: (FILING DATE: 08-SEP-: CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 22201-4714
APPLICATION NUMBER:
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                                                                08-SEP-1995
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  GB 9303988.1
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; ORIGINAL SOURCE: ; ORGANISM: Sac
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Best Local Similarity 65.2
Matches 519; Conservative
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: MITCHARD, LEONARD C
REGISTRATION NUMBER: 29,009
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acatgtcgacatactgacggacttcgacatcgagacgacggccaagtcaagccgctgcagcagct 448
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                                                            GGATGATGTGGTCTCTACAGGATCTGACATTATTATTGTTGGAAGAGGACTATTTGCAAA
                                                                              ggatgaggtcgtcagcgacggtaccgatgtgatcattgttggcagaggggctctttgacaa 928
                                                                                                                                    GACACCCGGTGTGGGTTTAGATGACAAGGGAGACGCATTGGGTCAACAGTATAGAACCGT
                                                                                                                                                      gaccccgggggttggcctggacgacaaaggagacggcctgggccagcagtaccgcacggt 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCACACGGTGTGGTGGGCCCAGGTATTGTTAGCGGTTTTGAAGCAGGCGGCAGAAGAAGT 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tycacacygcgtcaccygccccygtgtgatagccyggctgaaggaggctgcgaaactggc 628
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                                                      939 cccaaggtcgagggtgcccgctaccgcaaggccggttgggaggcttacttgcgccgtatg 998
                                                                                     295 ATTGGCAAACGAGGTTCCGATATCATCATTGTAGGTCGTGGCATAATCTCAGCAGCTGAT 236
                                                                                                    879 gtcagcgacggtaccgatgtgatcattgttggcagagggctcttttgacaagggaagagac 938
                                                                                                                                759 gcgcagcgtgacatgggtgggcgtgcagacggctttgactggctcatcatgaccccgggg 818
                                                                                                                                                                                                                        699 tataccgcgggcgtcgttgaaatggcgaagctggacgaagactttgtgatcgggttcatc 758
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                                                                                                         gcgcagcgtgacatgggtgggcgtgcagacggctttgactggctcatcatgaccccgggg
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  GTTCAGTTAGAAGCAGGAGGTGATAATCTCGGCCAGCAGTACCACAGCCCACAAGAAGTC
                       9tt9gcct9gacgacaaaggagacggcctgggccagcagtaccgcacggtggatgaggtc
                                                                                                                                                                   TACACTGAGGCAGCAGTGCAAATGGCTGAAGAACATTCTGAATTTGTGATTGGTTTTATT
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Contact: Lewin, H. A.
Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana,
61801, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi 9: Cross_match from Washington University Genome Center PHRAP suite. This sequence is vector free and at least 200 bp in length.
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Bovine ESTs
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Fax: 217 244 5617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-*Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NoLI; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. "

a 119 c 155 g 140 t 6 others
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/db_xref="taxon:9913"
/clone="BP250013A10B4"
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                           cagtactcctccggcgtgtaccgtatcgcggagtgggcggatattaccaatgcacacggc 578
                                                                                 CAGGAGTTCTTGATATTTGAAGACCGGTAGTTTGCAGATATAGGAAACACAGTGATAAAG
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High quality sequence start: 28
High quality sequence stop: 758.
Location/Qualifiers
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600944553T1 NIH_MGC_17
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Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortlum/LLNL at: image.l
Plate: LLCM54 row: 1 column: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
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                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                    /tissue_type="rhabdomyosarcoma"
/tissue_type="rhabdomyosarcoma"
/lab_host="DHIOB (phage=resistant)"
/note="organ: muscle; vector: pOTB7; Site_1: ECORI;
/note="organ: muscle; vector: pOTB7; Site_1: ECORI;
/note="organ: muscle; vector: pOTB7; Sites using the birectionally cloned into EcoRI/XhoI sites using the birectionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCAGCAG(G), Size-selected >500bp for average insert size 1.8kb. Library constructed by ting Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 268 c 188 g 248 t
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/db_xref="taxon:9606"
/clone="IMAGE:2960725"
/clone_lib="NIH_MGC_17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 to 987)
                                                                                                                                                                                      50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                  0;
                                                                                                                                                                  Score 86.4; DB
Pred. No. 4e-14;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens cDNA
                                                                                                                                                                                                             DB 106;
                                                                                                                                                                     251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 20-JUL-2000 clone IMAGE:2960725
                                                                                                                                                                     Indels
                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collection (MGC)
                                                                                                                                                                     18;
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                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             998
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                                                                                     638
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SOURCE
ORGANISM
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                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19
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Local Similarity 54.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTGGTCCTGGAATCGTGGATGGACTAAA 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   accggccccggtgtgatagccgggctgaa 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATGCAGGAGGGATCTTTCACATATTGGATTGGGCTCACATAGTAAATGCTCACATAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aacttcatgatcttcgaggaccgcaagttcgctgacattggcaacacggttaagctgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGCCTGATTTTACTCCTGATTTTGGCTCTAAGCTTCTCTCGA---TTGCAGAGAAACAT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ctgacggacttcgacatcgagacgacagtcaagccgctgcagcagcttgcggctaagcac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctggagctagcacgctgggaccgcacatttgtctgctgaagacacatgtcgacata 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atgcacgagaagaaaaccaatctctgcgcttcccttgatgtgcggacgtctagaaagctt 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCATTTGGGGAGAGGGCGAATCTGTCCAAGAATCCAACAGGAAAGAAGTTGTCCCAGATA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACTTCTTAATCTTTGAGGATCGTAAATTTGCTGACATTGGTAACACAGTAACCATGCAA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCGCTCAGAAGGAGAATCTGTGTTTGGCTGCAGATGTTGGAACTGCAGCTGAATTG 138
Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA166990 391 bp mRNA EST 19-DEC-1996 zp12e09.rl Stratagene fetal retina 937202 Homo sapiens cDNA common com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYNTHASE (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 391)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="root tips"
/dev_stage="harvested after 3 days of N-starvation"
/dev_stage="harvested after 3 days of N-starvation"
/note="vector: pBluescript pSK; Site_1: EcoRI; Site_2:
XhOI; Plants were grown in an aeroponic chamber for 14
days on nitrogen-rich medium followed by 3 days on N-free
medium. RNA was extracted from root tips (1-3 cm). CDNA
was prepared from polyA+ enriched RNA. The cDNA was
directionally ligated into Uni-zapXR vector from
Stratagene and packaged using Gigapack Gold packaging
extracts. Plasmids containing CDNA inserts were
mass-excised from phage stocks using ExAssit helper phage
and propagated in SOLR cells. Clone ordering and
sequencing was performed by the Centre National de
Sequencage (Genoscope, Evry, France)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       391 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 96.2; DB 28; Pred. No. 4.5e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 461;
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AA166990 RESULT

KEYWORDS VERSION 밁 Ş 밁 á В Ş 밁 Ş B ş ₽ á

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                                                                                                                           KEYWORDS
                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                      BF044448
                                                                                                                                                                                                                                                       RESULT
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                                                                                                                                                VERSION
                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                       COCUS
                                                                                          ORGANISM
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Best Local
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                                                                                                                                                                                                                                                                                                              390
                                                                                                                                                                                                                                                                                                                                                                                 330
                                                                                                                                                                                                                                                                                                                                            555 gc 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                   270 GAGTTGATAACTCTGGCAAAATGCCATGAGTTCTTGATATTTGAAGACCGGAAGTTTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 GCTGATGTTTCACTGGCCAGAGAGCTGTTGCAGCTAGCAGATGCTTTAGGACCTAGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93
                                                                                                                                                                                                                                                                                                              ရှ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgtctgctgaagacacatgtcgacatactgacggacttcgacatcgagacgacagtcaag 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATATAGGAAACACAGTGAAAAAAGCAGTATGAAGGAGGTATCTTTAAAATAGCTTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                  gacattggcaacacggttaagctgcagtactcctccggcgtgtaccgtatcgcggagtgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ccgctgcagcagcttgcggctaagcacaacttcatgatcttcgaggaccgcaagttcgct 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCATGCTGAAGACTCATGTAGATATTTTGAATGATTTTACTCTGGATGTGA----TGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAGTTGCATCGAAGCTTCTCAGGCTTATGCAAAAGAAGGAGACCAATCTGTGTCTATCT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ccagttgctagaaagcttctggcattgatgcacgagaagaaaaccaatctctgcgcttcc 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180;
                                                                                                                                                                          BF044448 570 bp mRNA EST 10-OCT-20
BP250013A10B4 Soares normalized bovine placenta Bos taurus
clone BP250013A10B4 5', mRNA sequence.
                                                                                                                         BF044448.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28M13 rev2 from Amersham
   Lewin, H.A.,
                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                        Bos taurus
                                                                                                            COW
                                                                                                                                                               BF044448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97044478
                                     Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                  (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Stratagene fetal retina 937202"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:609256"
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/db_xref="GDB:4624515"
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   Soares, M.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.6%;
                      570)
                                       Bos.
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   Rebeiz, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 119;
   Pardinas, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 391;
Liu, L.
                                                                                                                                                                                                                   10-OCT-2000
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                                                        Bovoidea
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Indels Length

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Gaps

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401

356

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RESULT 1
BE203967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: VandenBosch K
Department of Biology
Texas Asm University
College Station, TX 77843-3258, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
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             /tissue_type="Seedling roots"
/dev_stage="Immediately prior to inoculation with
Sinorhizobium meliloti (0 hour)"
/lab_host="E.coli strain XLOLLR"
/note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK -; Site_1: EcoRI; The cDNA
khoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
                                                                                                                                                                                                                  /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                                                /clone="pKV0-13J7"
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                                                                                                                                                                                                     Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire
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               /cultivar="Jemalong"
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Kahn,D., Gian
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291 aagaaaaccaatctctgcgcttcccttgatgtgcggacgtctagaaagcttctggagcta 350
                                                                                                                   231 ganagggccaaggcacacaattcgccagttgctagaaagcttctggcattgatgcacgag 290
                                                                                                                                                                                                                          Local Similarity
                                                             GAGAGGGCTAAGCTGTCGAAGAATCCAATGGGAAAGAGGTTGTTTGAGATAATGGCTGAG 87
                                                                                                                                                                                             215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
High quality sequence stop: 417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A., Bolla,B., Marra,M., Hillier,L., Kucabā,T., Martin,J., Beck,C. Wylle,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D:, Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R., and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
A. Rolla.B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE210781 465 bp mRNA EST 29-JUN-2000 so53604.y1 Gm-c1039 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1039-1687 5' similar to SW:PYR5_TOBAC Q42942 URIDINE 5'-MOOPHOSPHATE SYNTHASE ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabaceae; Papillonoideae; Glycine.
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314 286 1810
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBluescriptII SK+; Site_1: ECORI; Site_2: XhOI; This cDNA library was constructed from mRNA isolated from 2 week old seedlings with the cotyledons removed at the time of harvest. The seedlings for the cultivar Ogden were grown in a growth chamber using germination paper. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhOI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhOI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhOI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DHIOB host cells (Gibco BRL). This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="whole seedling without cotyledons"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="GENOME SYSTEMS CLONE ID: Gm-c1039-1687"
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                                                                                                                                                                                                                   7.6%;
                                                                                                                                                                                          ..
                                                                                                                                                                                                                   Score 104.8; DB 1
Pred. No. 1.4e-19;
                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                    DB 105;
                                                                                                                                                                                162; Indels
                                                                                                                                                                                                                                                Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                       Shoemaker."
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                                                                                                                                                                                       3; Gaps
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RESULT 1
AA802030
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ttcgacatcgagacgacagtcaagccgctgcagcattgcggctaagcacaacttcatg 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA802030 557 bp mRNA EST 25-NOV-1998 GM03750.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM03750 5prime similar to L00968: r-1 FBgn0003257 PID:9158794 SWISS-PROT:Q01637, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C., Brokstein,P., Lewis,S. and Rubin,G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Harvey,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BDGP/HHMI Drosophila EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                     Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
1 (bases 1 to 557)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fruit fly
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          128
                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 395.
                                                                                                                                                                                                                                                                                                                                                                                                                               LSA, Berkeley, CA 94720-3200, USA
510 643 9947
/note="Organ: ovary; Vector: BlueScript SK; Site_1: EcoRI; Site_2: XhoI; Constructed using Stratagene ZAP-cDNA Synthesis kit. Oligo dT-primed and directionally cloned at EcoRI and XhoI in BlueScript SK(+/-)"

152 c 166 g 111 t
                                                                                                                                /dev_stage="newly eclosed females: germarium·stage 6"
/lab_host="SOLR"
                                                                                                                                                                                 /sex="female"
                                                                                                                                                                                                      /clone_lib="GM Drosophila melanogaster ovary BlueScript"
                                                                                                                                                                                                                                   /clone="GM03750"
                                                                                                                                                                                                                                                          /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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Matches 191; Query Match Best Local Similarity

Conservative

0.

Indels Length 557;

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Gaps

<u>ب</u>

58.8%;

Score 99.4; DB 12; Pred. No. 5.5e-18; Mismatches 131;

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FEATURES
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ttctggagctagcacacctgggaccgcacatttgtctgctgaagacacatgtcgaca 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tgatgcacgagaagaaaaccaatctctgcgcttcccttgatgtgcggacgtctagaaagc 339
                                                                                                                               ATACAACTTCTGCAGTAAAAATTGCTGAGGATCATTCTGACTTTGTAATTGGCTTCATCT
                                                                                                                                                                     ataccgcgggcgtcgttgaaatggcgaagctggacgaagactttgtgatcgggttcatcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                acaacttcatgatcttcgaggaccgcaagttcgctgacattggcaacacggttaagctgc 519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tactgacggacttcgacatcgagacgacagtcaagccgctgcagcagcttgcggctaagc 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAATGGCTGAGAAGGAGAGTAATCTATGTTTGGCTGCTGATGTTGGAACTGCAGCTGAAT 71
                                                                                                                                                                                                                                                                                                                                                                  AATATGAAGGAGGGTTTTTCGTATATTGGATTGGGCTCATATAGTAAATGCTCACATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTCAGGTCCTGGAATTGTTGATGGATTAAAATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence stop: 428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I-Sal I restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into Endir ElectroMax DH10B host cells (Gibco BRL). This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna."

101 c 142 g 189 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a Not I restriction site. Sal I linker adapters were ligated to the blunt-ended cDNA fragments followed by Not I digestion. The cDNA fragments were directionally cloned into the No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        greenhouse grown plants. The library was prepared using the Life Technologies pSuperScript cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B (Gibco BRL)"
/note="Vector: pSPORT1 (Life Technologies); Site_1: Not Site_2: Sal I; This cDNA library was constructed from mR isolated from immature seed coats (200-300 mgs) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="immature seed plants"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="GENOME SYSTEMS CLONE ID: Gm-c1019-6395"
/clone_lib="Gm-c1019"
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/db_xref="taxon:3847"
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54.7%;
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Pred. No. 2.0
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                                                         AGTGACAATGCAAGCTGAAGGAGGTATCTTCCGCATTTTAGATTGGGCTGATGTAATTAA
                                                                             tgcggctaagcacaacttcatgatcttcgaggaccgcaagttcgctgacattggcaacac 508
                                                                                                                                                                                                                                               acatgtcgacatactgacggacttcgacatcgagacgacagtcaagccgctgcagcagct
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Magnoliophyta; eudicotyledons; core eudicots; Asteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 prime sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clemson University Genomics Institute
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864 656 4293
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                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="seedlings 5 days post-imbibition", note="Vector: pBlueScript SK(-); Site_1: EcoR1; xho1; supplier: Tanksley; Tissue supplied by Dav (USDA-ARS, Ithaca, NY 14850)."

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This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800

Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   info@genomesystems.com web site: www.genomesystems.com
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                                                cloned Pfu DNA polymerase, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the CDNA would be protected by their hemimethylated status. The CDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Strattagene's pBluescript II XR Predigested wettor (pBluescript II SK(+) that has been digested with EcoRI and XhoI, and phosporylated by Stratagene). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=25). This library was constructed by Dr. Paul Keim and Dr. Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      first-strand synthesis primer was used. An 'anchor' nucleotide (V-A,C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAGAGAGAGTCTCGAG(T)]18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with
                               library was constructed by Dr. Paul Keim and Coryell."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; The mRNA was isolated from roots of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were innoculated with Bradyrhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesize the the Lagrage synthesize the Lagrage cDNA was hemimethylated. A modification of Stratagene's
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/clone_lib="Gm-c1028"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 aagcttctggcattgatgcacgagaagaaaaccaatctctgcgcttcccttgatgtgcgg 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW704630 586 bp mRNA EST 18-APR-2000 sk54e06.yl Gm-c1019 Glycine max cDNA clone GENOME SYSTEMS CLOI Gm-c1019-6395 5' similar to SW:PYR5_TOBAC_Q42942 URIDINE 5'-MONOPHOSPHATE SYNTHASE; mRNA sequence.
This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                     Washington University School of Medicine
                                                                                                                                                                                                                            Contact: Shoemaker R/Public Soybean EST Project
                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Glycine.

1 (bases 1 to 586)
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                                                                                 Email: est@watson.wustl.edu
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                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 775)
                                                                                                                                                                                                                                                                                                                             mRNA sequence.
BE394063
                                                                                                                                                                                                                                                                                                                                                                    BE394063 775 bp mRNA
601312432F1 NIH_MGC_44 Homo
                                         Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                       Unpublished (1999)
                                                                                                           NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                Homo sapiens
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Procurement:
                   Robert_Strausberg@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, a poly(A) RNA were prepared, a cDNA library was made in TJ Close lab (Choi, Close, Fenton) at the University o California, Riverside. The cDNA clones were in vivo excised to give pBluescript phagemids before
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               normalization was carried out.
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DEFINITION BE019969

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TCTGAATTTGTG
                                                             gaagactttgtg
                                                                                                                               ACCGGCTCCCTGGCCACTGGGGACTACACTAGAGCAGCGGTTAGAATGGCTGAGGAGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                 GCAGATCTAGTAAATGCTCACGTGGTGCCAGGCTCAGGAGTTGTGAAAGGCCTGCAAG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATATAGGAAACACAGTGAAAAAGCAGTATGAAGGAGGTATCTTTAAAATAGCTTCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCATGCTGAAGACTCATGTAGATATTTTGAATGATTTTACTCTGGATGTGA---TGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTGATGTTTCACTGGCCAGAGAGCTG-TGCAGCTAGCAGATGCTTTAGGACCTAGTATC
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Plate: LLCM349 row: p column: 08
High quality sequence stop: 652.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.4%;
Similarity 56.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NH_MGC_44"
/clone_lib="NH_MGC_44"
/tissue_ltype="endometrium, adenocarcinoma cell line"
/tissue_ltype="endometrium, adenocarcinoma cell line"
/tissue_ltype="endometrium, adenocarcinoma cell line"
/lab_nost="PhiDB (phage=resistant)"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
/corgi; cDNA made by oligo-dT priming. Directionally
/cloned into EcoRI/XhoI sites using the following 5'
/cloned into EcoRI/XhoI sites using the following 5'
/adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
/pressure in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
/pressure in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
/pressure in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
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/db_xref="taxon:9606"
/clone="IMAGE:3659383"
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360 ctgggaccgcacatttgtctgctgaagacacatgtcgacatactgacggacttcgacatc 419
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                                                   AACCTCTGCGTCGCCGATGTTACAACAGCAAAGGAACTCCTTGAGCTAGCCAACAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Triticum aestivum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
1 (bases 1 to 579)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE405348 579 bp mRNA EST 21-JUL-2000 WHE1213_C11_E212S Wheat etiolated seedling root cDNA library Triticum aestivum cDNA clone WHE1213_C11_E21, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 seq primer: Strategene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., H., P.S., Hsla,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Olin Anderson
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                                                                                                                                                                                                                                                                                                      142
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                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5105595773
                                                                                                                                                                                                                                                                                         sequencing were performed in the OD Anderson lab (all other authors)."

140 c 150 g 147 t
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                                                                                                                                                                                                                                                                                                                                               California, Riverside.
sequencing were perfor
                                                                                                                                                                                                                                                                                                                                                                                              harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="Five day old etiolated seedling" /lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Root
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4565"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone-"WHE1213_C11_E21"
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                                                                                                                                                                     9,3%;
                                                                                                                                                Score 128.4; I
Pred. No. 2e-20
0; Mismatches
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2e-26;
                                                                                                                                                                                                                                                                                                                                                                              Plasmid DNA preparations and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      720 atggcgaagctggacgaagactttgtgatcgggttcatcgcg 761
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                                                                                                                                                                                                                                                                                                                                                                         quality sequence with phred score
Seq primer: Stratagence or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andérson,O.D., Chaó,S., Choi,D.W., Clóse,T.J., Fenton,R.D., H, P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US Department of Agriculture, Agriculture Research Service, Pacific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Olin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
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1 (bases 1 to 581)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5105595818
                       surface-sterilized, germinated and
                                            pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
                                                                                                /dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
                                                                                                                                                                                                                      /cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1455_H07_013"
                                                                                                                                                                                                                                                                                                  /organism="Triticum aestivum"
                                                                                                                                                  /tissue_type="Root"
                                                                                                                                                                                                 /clone_lib="Wheat etiolated seedling root normalized cDNA
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dark at room temperature on filter paper with water,
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                       grown aseptically in
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                                                                 GCTGCTGCCGTAAAAATTGCCGAACAACACTCCGATTTTGTCATCGGTTTCATCTC
                                                                                                                                   GGGCTGTTGCTACTTGCTGAAATGAGCTCTGCTGGTAACCTTGCCACGGGGGACTACACA
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                                                                                                                                                                                                                                                                                                                                              TTCATGATATTTGAAGACCGTAAATTTGCAGACATCGGTAACACAGTAACAATGCAGTAT
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                                                                                                                                                                                                        GGTCCTGGAATTGTTGATGGTTTGAAATTGAA----
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Upton, NY 11973, USA
Tel: 516-344-3396
Fax: 516-344-3407
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ESTs from developing cotton fiber
Unpublished (1999)
Contact: Ben Burr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gossypium hirsutum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biology Department
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: burr@bnlux1.bnl.gov
Seq primer: T3 Primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="Six days post anthesis"
/lab_host="%IX.Blue"
/note="vector: pBluescript II KS+"
/117 c 147 g 175 t 2
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/clone_lib="Six-day Cotton fiber"
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TCCAGGGCCAGGGATTATAGATGGCTTAAAACTCAA-----
                                              caccagaccccagatgtgatagccagagctgaaggaggctgcgaaactggcctcacaggaacc
                                                                                                                                            gtactcctccggcgtgtaccgtatcgcggagtgggcggatattaccaatgcacacggcgt
                                                                                                                                                                                                                        CAACTTTTTGATTTTTGAGGATAGGAAGTTTGCTGATATAGGTAACACAGTTACCATGCA
                                                                                                                                                                                                                                                   caacttcatgatcttcgaggaccgcaagttcgctgacattggcaacacgggttaagctgca
                                                                                                                                                                                                                                                                                                                                     CTATCCTGATTTCACTCCTGATTTTGGTGCAAA---GCTGAGGCTGATTGCAGACAAGCA
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                                                                                                            GTATGAAGGTGGTCTTTTCAAGATTGTAGAGTGGGCAGACATTGTAAATGCACACATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATGGAGCAGAAAAAGAGTAATCTTTCACTTGCTGCAGATGTGAATTCTGCTGCTGACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biology Building, Room 16, Austin, Tel: 512 471 4238
Fax: 512 232 3402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE641945 820 bp mRNA EST 01-SEP-2000 Cri2_4_L06_SP6 Ceratopteris Spore Library Ceratopteris richardii cDNA clone Cri2_4_L06 5', mRNA sequence.
BE641945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: sroux@uts.cc.
Plate: Cri2_4 row:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Section of Molecular Cell and Developmental University of Texas
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Expressed sequence tags of cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Filicopsida; Filicales; Pteridaceae; Ceratopteris.
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/note="Vector: pcMVSPORT6; EST sequence from cDNA library.
cDNA library constructed from mRNA isolated from C.
richardii spores that had developed for 20 hours after
their germination had been initiated by white light."
a 159 c 219 g 210 t
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/cell_type="Gametophyte"
/dev "Coll_type="Spore"
/dev 
/dev <p
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/clone_lib="Ceratopteris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Ceratopteris richardii"
/cultivar="Brogn"
/db_xref="taxon:49495"
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Pred. No. 3.4e-27;
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om a C. richar
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1117: em_estp16:*
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1121: em_estp1014:*
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1189: em_gss1:*
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9	S	191:	S
_gss28:	b_gss27:	b_gss26	b_gss25:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

	55.8 4.0 276 6 AA384977 AA384977	19 30.0 4.1 273 ANESTOCO ALESTOCO ALEST	8 57.8 4.2 564 23 AI668476 AI668476 AA295675	37 57.8 4.2 516 93 AW659213 AW65921	5 59.6 4.3 153 96 AW851587 AW85158	4 59.8 4.3 809 135 BE745374 BE74537	3 60 4.3 777 140 C97586 C97586	2 60.6 4.4 117 96 AW851496 AW851496	0 65 4.7 148 96 AW851491 AW851491	9 66.8 4.8 719 26 AI894226 AI894226	8 67 4.9 247 5 AA329585 AA329585 E	27 70.8 5.1 591 89 AW360558 AW360558	6 74.2 5.4 668 138 BE951337 BE95133	5 74.4 5.4 724 96 AW905992 AW905992	4 74.6 5.4 431 2 AA125810 AA125810 z	. 23 75 5.4 649 40 AW116069 . AW116069	2 79.2 3.7 345 34 AW/33033 AW/98792	0 79.6 5.8 698 39 AWURD	9 80.8 5.9 918 109 BE542503 BE54250	8 84.2 6.1 420 2 AA128100 AA128100	7 85.4 6.2 550 14 AA944506 AA94450	6 86.2 6.2 328 31 AV168581 AV168581	15 86 4 6 3 987 106 BE300085 BE30008	3 95.6 6.9 391 3 AALOO990 AALOO990	2 96.2 7.0 461 28 AL369478 AL369478	97.4 7.1 610 105 BE203967 BE203967	99.4 7.2 557 12 AA802030 AA802030	104.8 7.6 465 105 BE210781 BE21078	107.2 7.8 639 93 AW626116 AW62611	107.4 7.8 586 94 AW704630 AW704630	107.6 7.8 557 133 BE019969 BE01996	116 9 4 775 107 BE30406	128.4 9.3 579 107 BE405348 BE40534	131.2 9.5 820 110 BE641945 BE64194	136.4 9.9 597 24 AI731663 AI73166	core Match Length DB ID Descript
BE470313 IpHdk I326762 mq67f0	862776 wj96d08	597621 tn15g0	1668476 605032	W659213 96179	W851587 IL3-	E745374 6015	C97586 C97586 Ric	W851496 IL3-CT	537389 WEARCOS F	94226 md168	329585 EST3320	W360558 687067	951337 UI-M-CC	905992 E	25810 zl15a04.r	W116069 f106a04	792 ga01d05.	899 s110f09.	2503 6010638	28100 zl15a04.s	944506 EST2000	581 AV168581	E300085 60094455	044448	69478 MEBAJIL	E203967	802030 GM03750.5	210781 so53e04	26116 EST320	704630 sk54e06.y	E019969 sm38b04.	E44000	E405348 WHELZIS_	E641945 Cri2_4_L	3:1663	escript

ALIGNMENTS

RESULT

SOURCE uplan	KEYWORDS EST.	VERSION AI731	ACCESSION AI731663	to UR	DEFINITION BNLGH	LOCUS AI731663	AI731663
upland cotton.		AI731663.1 GI:5050515	663	to URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP, mRNA sequence	BNLGHil0421 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar	663 597 bp mRNA	
				TE SYNTHASE (UMP, mRNA	n fiber Gossypium hirs	RNA EST	
				sequence.	utum cDNA 5' similar	11-JUN-1999	

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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1380
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Copyright (c) 1993 - 2000 Com
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Listing first 45 summaries
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1380
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                                                                                        glabrata
Gene 142,
                                                                                                                                                                                            L13661.1 GI:388364 orotidine-5'-phosphate decarboxylase. Candida glabrata (strain 85/038) DNA. Candida glabrata
                                                                                                                                                                Eukaryota; Fungi; Ascomycota;
anamorphic Saccharomycetales;
                                                                                                                                                                                                                                                                                          Candida glabrata orotidine-5'-phosphate
                                                                                                                      A system for gene
                                                                                                                                       Zhou, P.,
                                                                                                                                                                                                                                                                            complete cds
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                                                                                                                                                   (bases 1 to 1021)
                                                                                                                                Szczypka, M.S., Young, R.J. and Thiele, D
              /organism="Candida glabrata"
/strain="85/038"
/db_xref="taxon:5478"
                                                           Location/Qualifiers
                                                                                        135-140 (1994)
                                                                                                                                                                                                                                                                                                          1021 bp
                                                                                                                     cloning and
                                                                                                                      manipulation in the yeast Candida
                                                                                                                                                                   Candida.
                                                                                                                                                                                Saccharomycetes;
                                                                                                                                                                                                                                                                                          decarboxylase
                                                                                                                                                                                  Saccharomycetales
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/product-"orotidine-5'-phosphate decarboxylase"
/protein_id="AAA34325.1"
/protein_id="AAA34325.1"
/db_xref="G1:388365"
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/translation="MSSASYLQRAEAHPSPVASKLMHEKTNLCASLDVTTSel"
/translation="MSSASYLQRAEAHPSPVASKLLK"
/translation="M
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/EC_number-"4.1.1.23"
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TAACACAGTCAAATTACAATATACATCGGGCGTTTTACCGTATCGCAGAATGGTCTGATAT
                 caacacggttaagctgcagtactcctccggcgtgtaccgtatcgcggagtgggggtat
                                                                                gcagcttgcggctaagcacaacttcatgatcttcgaggaccgcaagttcgctgacattgg
                                                                                                                              GAAAACACACGTTGATATCTTGGATGATTTCAGTTATGAGGGTACTGTCGTTCCATTGAA
                                                                                                                                                                gaagacacatgtcgacatactgacggacttcgacatcgagacgacagtcaagccgctgca
                                                                                                                                                                                                 TCGTTCGACTGATGAGCTATTGAAACTTGTTGAAACGTTGGGTCCATACATTTGCCTTTT
                                                                                                                                                                                                                                                                 ATCGAAACTTTTACGTTTAATGGATGAAAAGAAGACCAATTTGTGTGCTTCTCTTGACGT
                                                                                                                                                                                                                                                                                                                                   TTGCACCATGTCCACAAAATCATATACCAGTAGAGCTGAGACTCATGCAAGTCCGGTTGC
                                                                AGCATTGGCAGAGAAATACAAGTTCTTGATATTTGAGGACAGAAAATTCGCCGATATCGG
                                                                                                                                                                                                                                                                                                                                                                                                   527;
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Shuster, J.R., Moyer, D. and Irvine, B.
Sequence of the Kluyveromyces lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (24-NOV-1987) Shuster J.R.,
Horton Street, Emeryville, CA 94608 U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shuster, J.R.
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Kluyveromyces lactis.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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/db_xref-"taxon:28985"
178. .981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MSTKSYTSRAETHASPVASKLIRLMDEKKTINLCASIDVRSTDEL
KILVETLGPYICLLKTHYDILDDFSYEGTVPPLKALAKYKFLIFEDKKFADIGNTVK
LQYTSGYYRLAEWSDITNAHGYTGAGIVAGLKQGAQEVTKEPRGLLMLELSSKGSLA
HGEYTKGTYDIAKSDKDFVIGFIAQNDMGGREEGFDWLIMTPGVGLDDKGDALGQQYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAA68509.1"
/db_xref="GI:2906"
/db_xref="SWISS-PROT:P07922"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="decarboxylase (AA 1-267)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Pred. No. 2.3e-72;
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                                                                                                                                                                                                                                                                                                                                                                                     Isolation and nucleotide sequence analysis of the 5'-phosphate decarboxylase) gene of Kluyveromyces Agric. Biol. Chem. 52, 3067-3071 (1988)
Transcription of URA3 of K. lactis begins around -
       284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetaceae; Kluyveromyces.

1 (bases 1 to 1764)
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Yeast orotidine 5'-phosphate decarboxylase (URA3)
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Kluyveromyces lactis
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D00431.1 GI:218526
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553 a 327 c 385 g
bp upstream of XhoI site.
                                                                                                                                                                                                                                                                                                                                                                        nscription of URA3 of K. lactis begins around -30 to -40 from initiation ATG codon. It was identified by S1 mapping.
                                                                                                                                                                                                                                              /note=
                                      TVDEVVSGGSDIIIVGRGLFAKGRDPKVEGERYRNAGWEAYQKRISAPH
                                                                                                                                                                                                            /note="putative" 499. .1302
                                                                                                                                                                                                                                                                               /organism="Kluyveromyces lactis"
/db_xref="taxon:28985"
207. .214
                                                     /translation="MSTKSYTSRAETHASPVASKLLRLMDEKKTNLCASLDVRSTDEL
LKLVETLGPYICLLKTHVDILDDFSYEGTVVPLKALAEKYKFLIFEDRKFADIGNTVK
LQVTSGVYRIAEMSDITNAHGVTGAGIVAGLKQGAQEVTKEPRGLLMLAELSSKGSLA
HGEYTKGTVDIAKSDKDFVIGFIAQNDMGGREEGFDWLIMTPGVGLDDKGDALGQQYR
                                                                                                                                  /protein_id="BAA00333.1"
/db_xref="GI:218527"
                                                                                                                                                                                     /note="orotidine 5'-phosphate decarboxylase"
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                                                                                                 CGCCAAGGGTAGAGATCCTAAGGTTGAAGGTGAAAGATACAGAAATGCTGGATGGGAAGC
                                                                                                                tgacaagggaagagaccccaaggtcgagggtgcccgctaccgccaaggccggttgggaggc
                                                                                                                                                                       cacggtggatgaggtcgtcagcgacggtaccgatgtgatcattgttggcagagggctctt
                                                                                                                                                                                                                                 catcatgaccccgggggttggcctggacgacaaaggagacggcctgggccagcagtaccg
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Pred. No. 2.2e-72;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungl; Ascomycota; Saccharomycetes; anamorphic Saccharomycetales; Candida.
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JP 1996173170-A/3
09-JUL-1996
28-APR-1995 JP 1995129287
25-MAY-1994 JP 94P 135019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISAWA NORIHIKO, KONDO KEIJI, 26-OCT-1994 JP 94P CI2N15/09,C07H12/04,C12N1/19,(C12N1/19,C12R1:72); Strandedness: Double; topology: 140cc.
                                                                                                                                                                                                                                                                caacgaaatcttacgcagaaagggccaaggcacacaattcgccagttgctagaaagcttc
                                                                                                                                                                            gaaagcttctggagctagcagacacgttgggaccgcacatttgtctgctgaagacacatg 393
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acggcgtcaccggccccggtgtgatagccgggctgaaggaggctgcgaaactggcctcac
                                            agctgcagtactcctccggcgtgtaccgtatcgcggagtgggcggatattaccaatgcac
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                                AGGCACAGTACGCCGGTGGTGCGTTCAAGATTGCGCAATGGGCAGATATCACCAACGCCC
                                                                           AGAAGCACAATTTCCTCATCTTTGAGGACCGTAAGTTTGCTGATATCGGCAACACCGTCA
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/db_xref="taxon:4961"
/organism="Candida utilis"
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            ctaagcacacttcatgatcttcgaggaccgcaagttcgctgacattggcaacacggtta
                                                                                                          gaaagcttctggagctagcagacacgctgggaccgcattttgtctgctgaagacacatt
                                                                                                                                                                  TTTCGCTTATGGAGTCCAAGAAGACGAACCTGTGTGCCAGTGTCGATGTTCGTACCACAG 1385
                                                                                                                                                                                tggcattgatgcacgagaagaaaaccaatctctgcgcttcccttgatgtgcggacgtcta
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                                                                   tcgacatactgacggacttcgacatcgagacgacagtcaagccgctgcagcagcttgcgg 453
                                                      TTGATATCATTGATGACTTCTCTATGGAGTCTACTGTGGCTCCACTGTTGGAGCTTTCAA
                                                                                                                                                                                                                                                                            521;
                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 2330)
Kondo,K., Kajlwara,S. and Misawa,N.
Transformation systems for the yeast candida
expression of heterologous genes therewith
Patent: US 5849524-A 3 15-DEC-1998;
Location/Qualifiers
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Molecular Biology, Free University Amsterdam,
Amsterdam, NL-1081 HV, Netherlands
Location/Qualifiers
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Bergkamp,R.J., Geerse,R.H., Verbake
Cloning and sequencing of the URA3
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Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
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                                   AGGTGCCGAGGAAGTTACGAAAGAACCTAGAGGGTTGTTAATGCTTGCCGAGTTATCGTC
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1 (bases 1 to 1469)
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LRLVEVLGPYTCLLKTHYDLIEDESEENTIVPLKQLAEKHKFLIFEDEKFADIGNTVK
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HGEYTRGTVELAKSDKOFVIGETAQNDMGREEGYDKLIMTFGVGLDDKGDALGQQYR
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decarboxylase; URA3 gene.
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1123. .:
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LALVEKLAPYICWKTHIDIVSDFSYEGTVVPLVALAKKHFELLEDRKFADIGWTVK
HQYAGGVYQIARWADITNAHGVTGAGIVAGLKQAAEETTSEPRGLLMLAELSSKGAIA
HGKYTEETVEIAKTDKEFVFGFIAQDWGGREEGETWVVMTPGVGLDDTGDALGQQYR
TVDTYVQTGTDVIIVGRGLEGKGRHPAVEGERYRKAGWDAYTKRVSP"
                              coding sequence
                                                cerevisiae F100) URA3 gene coding
 GI:172061
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gcgcggaqactataccgcgggcgtcgttgaaatggcgaagcttggaacgaagactttgtgat
                                                                                  ctcacaggaacccagggggttgctgatgctggcagagctctcttctctcagggctcttttggc
                                                                                                                                                                                                                        AGTCAAATTGCAGTACTCTGCGGGTGTATACAGAATAGCAGAATGGGCAGACATTACGAA
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                                                           AACAAAGGAACCTAGAGGCCTTTTGATGTTAGCAGAATTGTCATGCAAGGGCTCCCTAGC
                                                                                                                                        TGCACACGGTGTGGTGGGCCCAGGTATTGTTAGCGGTTTGAAGCAGGCGGCGGAAGAAGT
                                                                                                                                                             tgcacacggcgtcaccggccccggtgtgatagccgggctgaaggaggctgcgaaactggc
                                                                                                                                                                                                                                                                                                       ATCCGCCAAGTACAATTTTTTACTCTTCGAAGACAGAAAATTTGCTGACATTGGTAATAC
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85028421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   orotidine-5'-phosphate decarboxylase; promoter region S.cerevisiae (strain FL100) DNA, 13kb EcoRI fragment.
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188 c 276 g 326 t
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LELVERAGPKICLKTHVDLLTDFSMEGTVSKPLKALSAKYNFLLEEDRKRADIGWYVK
LQYSAGVYRIAEWADITUAHGVVGPGTVSGLKQAAEEVTKEPRGLLMLAELSCKKSLA
TGEYTKGTVDIAKSDKDFVIGFIAQRDMGGRDEGYDMLIMTPGVGLDDKGDALGQOYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAA34825.1"
/db_xref="GI:172062"
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/db_xref="taxon:4932"
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65.7%;
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Pred. No. 2.3e-69;
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Cloning vector pDR1149
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AF106619.1 GI:4324617
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Hurst, S.T. and Rivier, D.H.
Direct Submission
Submitted (13-NOV-1998) CSB, University of Illinois
Urbana-Champaign, 601 South Goodwin Avenue, Urbana,
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Identification of a compound origin of replication locus in Saccharomyces cerevisiae
J. Biol. Chem. 274 (7), 4155-4159 (1999)

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/specific host="Saccharomyces cerevisiae"
/db_xref="taxon:88758"
1374. .1540
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1550. .2651
/note="URA3 sequence"
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                          2 (bases 1 to 4342)
ROSS-Macdonald, P.B.
Direct Submission
Submitted (12-APR-1996) Petra B. Roundersity, PO Box 208103, New Have
Location/Qualifiers
ie 1.4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGATGATGTGGTCTCTACAGGATCTGACATTATTATTGTTGGAAGAGGACTATTTGCAAA
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                                                                                                                                     1 (bases 1 to 4342)
Ross-Macdonald,P., Sheehan,A., Roeder,G.S. and Snyder,M.
A multipurpose transposon system for analyzing protein production, localization, and function in Saccharomyces cerevisiae
Proc. Natl. Acad. Sci. U.S.A. 94 (1), 190-195 (1997)
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(GFP), OMP decarboxylase (URA3), and tetracycline
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APFLAAAVLNGLNLLLLGCFLMQESHKGERRPMPLRAFNPVSSFRWARGMTIVAALMTV
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4161. .4194
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KQAIIAGMAADALGYVLLAFATRGWMAFPIMILLASGGIGMPALQAMLSRQVDDDHQG
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/db_xref="GI:1335940"
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/transl_table=11
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2684. .3874
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LQYSAGVYRIAEMADITNAHGVVGPGIVSGLKQAAEEVTKEPRGLLMLAELSCKGSLA
TGEYTKGTVDIAKSDKDFVIGFIAQRDMGGRDEGYDWLIMTPGVGLDDKGDALGQQYR
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                                                                                        rpt_type=terminal
1014 c 1084 g
                                                                                                                                                                                                                                              /transl_table=11
                                                                                                                                                                                                                                                                                             /note="from influenza virus"
                                                                                                                                                                                                                                                                                                                                    /note="loxP site"
/organism="synthetic construct"
                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Tn3 res site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="OMP decarboxylase"
/protein_id="AAB01174.1"
/db_xref="GI:1335939"
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1688. .2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="green fluorescent protein"
/protein_id="AAB01173.1"
/db_xref="GI:1335938"
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135. .851
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/transl_table=11
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synthetic construct artificial sequence.
1 (bases 1 to 6107)
                                                                                      SCU54829 6107 bp DNA SYN 21-DEC-19
Synthetic E. coli Tn3-derived transposon OMP decarboxylase
and tetracycline efflux protein (tet) genes, complete cds,
beta-galactosidase (lacZ) gene, partial cds.
U54829
U54829.1 GI:1335931
                                                       synthetic construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ross-Macdonald, P., Sheehan, A., Roeder, G.S. and Snyder, M.
A multpurpose transposon system for analyzing protein production,
localization, and function in Saccharomyces cerevisiae
proc. Natl. Acad. Sci. U.S.A. 94 (1), 190-195 (1997)
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LSGQTTEVTSEYLFRHSDNELLHWMVALDGRPLASGEVPLDVAPQGKQLIELPELPQP
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FCIELGNKRWQFNRQSGFLSQMWIGDKKQLLTPLRDQFTRAPLDNDLGVSEATRIDPN
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QMAITVDVEVASDTPHPARIGLNCQLAQVAEBVNWLGLGPQENYPDRUTAGGFDRWDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FHVATRENDDES RAVLEAEVQMCGELRDYLRVTVSLWQGETQVASGTAPEGGE I I DER GGYADRYTLRLWYENEXLWSAEI PHLY RAVVELHTADGTLIEAEACDVGFREVRI ENG LLLLLNGK PLLI RGVNRHEHPPLHGQVMDEQTMVQDILLKQNNFNAVRCSHY PNHPLW YTLCDRYGLYVVDEANI ETHGWPMNRLTDDPFWLPAMSERVTRWYQRDRNHESVI I W SLGNESGHGANHDALYRWIK SVDPSRPVQYEGGGADTTATD I I CPMYARVDEDQPFPA VPKWS I KKWLSLPGETRPLI LCEYAHAMGNSLGGFAKYWQAFRQYPRLOGGFVNDWVD
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LRSLNGEWRFAMFDAFBLYBLECDLDFBADTVVPSWQMHGYDAFIYTNVTYPIT
VNPPFVPTBHYGGYSLFENDESWLDGGQTRIIFDGVNSWQMHLWGNGRWYGYGQDSR
LPSEFDLSAFLRAGENRLAVMVLRWSDGSYLEDQDMWRMSGIFRDVSLLHKPTTQISD
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/db_xref="GI:1335932"
/translar4~~ ""
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                                                                              TVDDVVSTGSDIIIVGRGLFAKGRDAKVEGERYRKAGWEAYLRRCGQQN"
                                                                                                                                      /translation="mSkatykeraathpSpvaaklfnImHeKQTnlCASLDvrttkEL
LELVEALGPKICLLKTHVDILTDFSMEGTVKPLKALSAKYNFLLFEDRKFADIGNTVK
LQYSAGVYRIAEWADITNAHGVVGPGIVSGLKQAAEEVTKEPRGLLMLAELSCKGSLA
                                                                                                                                                                                                                        /product="OMP decarboxylase"
/protein_id="AAB01170.1"
/db_xref="GI:1335934"
                                                                                                                                                                                                                                                                                                                                                              /gene="URA3"
/note="Ura3p from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLSDMYTPYVFPSENGLRCGTRELNYGPHQWRGDFQFNISRYSQQQLMETSHRHLLHA
EEGTWLNIDGFHMGIGGDDSWSPSVSAEFQLSAGRYHYQLVWCQK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAB01169.1"
/db_xref="GI:1335933"
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/gene="lacz"
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                                                                                                               TGEYTKGTVDIAKSDKDFVIGFIAQRDMGGRDEGYDWLIMTPGVGLDDKGDALGQQYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="beta-galactosidase"
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                          /gene="tet"
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                                                                      3872 AACAAAGGAACCTAGAGGCCTTTTGATGTTAGCAGAATTGTCATGCAAGGGCTCCCTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 gcttctggcattgatgcacgagaagaaaaccaatctctgcgcttcccttgatgtgcggac 328
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gcgcggagactataccgcgggcgtcgttgaaatggcgaaggttggacgaagactttgtgat 748
                                                                                                ggttaagctgcagtactcctccggcgtgtaccgtatcgcggagtgggcggatattaccaa 568
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                                                                                                                                                                TGCACACGGTGTGGTGGGCCCAGGTATTGTTAGCGGTTTGAAGCAGGCGGCGGAAGAAGT 3871
                                                                                                                                                                                       tycacacggcgtcaccggccccggtgtgatagccgggctgaaggaggctgcgaaactggc 628
                                                                                                                                                                                                                                                       AGTCAAATTGCAGTACTCTGCGGGTGTATACAGAATAGCAGAATGGGCAGACATTACGAA
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RIVAGITGATGAVAGAYIADITDGEDRARHFGLMSACFGVGMVAGPVAGGLLGAISLH
APFLAAAVLNGLNLLLGCFLMQESHKGERRPMPLRAFNPVSSFRWARGMTIVAALMTV
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/protein_id="AAB01171.1"
/db_xref="GI:1335935"
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/protein_id-"AAB01172.1"
/db_xref-"GI:1335936"
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1571 c 1662
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/organism="synthetic construct"
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65.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGCTTTATTGCTCAAAGAGACATGGGTGGAAGAGATGAAGGTTACGATTGGTTGATTAT 4051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A multipurpose transposon system for analyzing protein production, localization, and function in Saccharomyces cerevisiae Proc. Natl. Acad. Sci. U.S.A. 94 (1), 190-195 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCU54828 6119 bp DNA SYN 21-DEC-1999 Synthetic E. coll Tn3-derived transposon OMP decarboxylase (UR. and tetracycline efflux protein (tet) genes, complete cds, and beta-galactosidase gene (lacz), partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (12-APR-1996) Petra B. Ross-Macdonald, Biology, Yale University, PO Box 208103, New Haven, CT 06520-8103, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    artificial sequence.
1 (bases 1 to 6119)
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                               /Translation-"DPVVLQRRDWENPGVTQLNRLAAHPPFASWRNSEEARTDRPSQQ
/TRSLNGEWRFAWFPAFBEAVPESWLECDLPEADTVVVPSNWQMHGYDAPIYTNVTYPIT
VNPPFVPTENPTGCYSLTFNVDESWLQGEQTTRIFOCYNSAFHAWCNGSWVGYQQDSR
LPSEFDLSAFLRAGENRLAVMVLWSDGSYLEDODMWRWSGIFRDVSLTHKPTTQISD
FHVATRENDDFSRAVLEAEVQMCGELRDYLRVTVSLWQGETQVASGTAPFGGEIIDER
GGYADRVTLRLWVENPKLWSAEIPNLYRAVVELHTADGTLIBAEACDVGFREVRIENG
                                                                                                                                                                                                                                   <135. .3188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                   construct"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 construct"
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BASE COUNT
                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                      Query Match
                                                                             3464 CATGTCGAAAGCTACATATAAGGAACGTGCTGCTACTCCTAGTCCTGGTGCTGCCAA 3523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
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                                                                                                                                                                                                                                                                                                                                                                                             repeat_unit
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269 gcttctggcattgatgcacgagaaagaaaaccaatctctgcgcttcccttgatgtgcggac 328
                                                                                                                                      209
                                                                                                                                                                                                              Local
                                                                                                                        catgicaacgaaatcitacgcagaaagggccaaggcacacaattcgccagtigctagaaa 268
                                                                                                                                                                                         523;
                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                          1445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLGNESGHGANHDALYRWIKSVDPSRPVQYEGGGADTTATDIICPMYARVDEDQPFPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4461.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .5651
                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                  1666 g
                                                                                                                                                                                                            Pred.
                                                                                                                                                                                                                                 Score 359.2;
                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                            No. 1.9e-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cerevisiae"
                                                                                                                                                                                                                                 DB 12;
                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                 Length 6119;
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